

SEQUENCE LISTING

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<140> PCT/GB2004/005325

<141> 2004-12-20

<150> GB 0329684.5

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<151> 2003-12-22

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<170> PatentIn version 3.1

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Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe	50	55	60
Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr	65	70	75
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Ala Ser Ile Ser Asp Gly Gly Ser Tyr Thr Tyr Tyr Pro Asp Asn Val	50	55	60	

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Asn Leu Tyr
65 70 75 80

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35 40 45

Gly Gln Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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35 40 45

Pro Gln Leu Leu Ile Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Ser
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35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
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Pro Gln Leu Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro
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Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile

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70

75

80

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<223> Murine gamma 2b constant region reverse primer

<400> 76

ggatcccggg agtggataga ctgatgg

27

<210> 77

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> Murine kappa constant region reverse primer

<400> 77
ggatcccggg tggatggtgg gaagatg 27

<210> 78

<211> 52

<212> DNA

<213> Artificial sequence

<220>

<223> 2A10 VH forward primer

<400> 78
actcataagc ttgccacat gggatggagc tgtatcatcc tctttttggt ag 52

<210> 79

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> VH reverse primer

<400> 79
actatgacta gtgtgccttg gccccagtag 30

<210> 80

<211> 42

<212> DNA

<213> Artificial sequence

<220>

<223> VL forward primer

<400> 80
actcataagc ttgccacat gaggtgctct cttcagtttc tg 42

<210> 81

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> VL reverse primer

<400> 81

actatgcgta cgtttcagct ccagcttgg

29

<210> 82

<211> 19

<212> PRT

<213> Artificial sequence

<220>

<223> CAMPATH-1H signal sequence

<400> 82

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser

<210> 83

<211> 120

<212> PRT

<213> Homo sapiens

<400> 83

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Gln Trp Leu Val Ile Leu Asn Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 84

<211> 113

<212> PRT

<213> Artificial sequence

<220>

<223> Humanised VH construct H1

<400> 84

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35

40

45

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Ser Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Glu Leu Gly Gln Gly Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 100 105 110

Ser

<210> 85

<211> 112

<212> PRT

<213> Homo sapiens

<400> 85

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
 1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Gly Leu Val Tyr Ser
 20 25 30

Asp Gly Asp Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
 35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Arg Asp Ser Gly Val Pro
 50 55 60

Asp Arg Phe Ser Gly Gly Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
 85 90 95

Thr His Trp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 86

<211> 112

<212> PRT

<213> Artificial sequence

<220>

<223> Humanised VL construct L11

<400> 86

Asp Ile Val Ile Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Tyr Lys
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Gly Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu
85 90 95

Val Glu Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 87

<211> 201

<212> PRT

<213> Homo sapiens

<400> 87

Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser Phe Glu
1 5 10 15

Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu
20 25 30

Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val Ile Gln
35 40 45

Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu Ser Ile
50 55 60

Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met Ser Val
65 70 75 80

Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu Pro Glu
85 90 95

Asn Ile Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile Ser Ile
100 105 110

Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro Ala Pro
115 120 125

Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro Val Pro
130 135 140

Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu Pro Val
145 150 155 160

Asp Leu Phe Ser Asp Asp Ser Ile Pro Asp Val Pro Gln Lys Gln Asp
165 170 175

Glu Thr Val Met Leu Val Lys Glu Ser Leu Thr Glu Thr Ser Phe Glu
180 185 190

Ser Met Ile Glu Tyr Glu Asn Lys Glu
195 200

<210> 88

<211> 462

<212> PRT

<213> Artificial sequence

<220>

<223> anti-NOGO antibody heavy chain

<400> 88

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Ser Tyr Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn
65 70 75 80

Glu Lys Phe Lys Ser Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
85 90 95

Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Glu Leu Gly Gln Gly Tyr Trp Gly Gln Gly Thr Leu Val
115 120 125

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
130 135 140

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
145 150 155 160

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
165 170 175

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
180 185 190

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
195 200 205

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
210 215 220

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
225 230 235 240

Cys Pro Pro Cys Pro Ala Pro Glu Leu Ala Gly Ala Pro Ser Val Phe
245 250 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
260 265 270

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
275 280 285

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
290 295 300

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
305 310 315 320

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
325 330 335

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
340 345 350

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
355 360 365

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
370 375 380

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly

385 390 395 400

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
405 410 415

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
420 425 430

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
435 440 445

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 89

<211> 238

<212> PRT

<213> Artificial sequence

$\langle 220 \rangle$

<223> anti-NOGO antibody light chain

<400> 89

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Asp Ile Val Ile Thr Gln Ser Pro Leu Ser Leu Pro Val
20 25 30

Thr Leu Gly Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu
35 40 45

Leu Tyr Lys Asp Gly Lys Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro
50 55 60

Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Met Ser Thr Arg Ala Ser
65 70 75 80

Gly Val Pro Asp Arg Phe Ser Gly Gly Gly Ser Gly Thr Asp Phe Thr
85 90 95

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys
100 105 110

Gln Gln Leu Val Glu Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu
115 120 125

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
130 135 140

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145 150 155 160

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
165 170 175

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
180 185 190

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
195 200 205

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
210 215 220

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 90

<211> 1428

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide encoding SEQ ID NO: 88

<400> 90

aagctttaca gttactcagc acacaggacc tcaccatggg atggagctgt atcatcctct 60

tcttggtagc aacagctaca ggtgtccact cccaggtgca gctggtgcag tctggggctg 120

aggatgaagaa gcctggggcc tcagtgaagg tttcctgcaa ggcattctgga tacaccttca	180
ccagctactg gatgcactgg gtgcgacagg cccctggaca agggcttgag tggatgggaa	240
atattaatcc tagcaatggg ggtactaact acaatgagaa gttcaagagc agagtcacca	300
tgaccagggg cacgtccacg agcacagtct acatggagct gagcagcctg agatctgagg	360
acacggccgt gtattactgt gaactgggac agggctactg gggccagggg aactagtca	420
cagtctcttc agcctccacc aaggggccat cggctcttccc cctggcacc cctccaaga	480
gcacctctgg gggcacagcg gccctgggct gcctgggcaa ggactacttc cccgaaccgg	540
tgacgggtgc gtggaaactca ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc	600
tacagtcttc aggactctac tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg	660
gacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag gtggacaaga	720
aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccc gacactgaac	780
tcgcgggggc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc ctcatgatct	840
cccggacccc tgaggtcaca tgcgtgggtg tggacgtgag ccacgaagac cctgagggtca	900
agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag ccgcgggagg	960
agcagtacaa cagcacgtac cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc	1020
tgaatggcaa ggagtacaag tgcaagggtct ccaacaaagc cctcccagcc cccatcgaga	1080
aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc ctgcccccat	1140
cccgggatga gctgaccaag aaccagggtca gcctgacctg cctgggtcaaa ggcttctatc	1200
ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac tacaagacca	1260
cgcctcccggt gctggactcc gacggctcct tcttctctta cagcaagctc accgtggaca	1320
agagcagggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag gctctgcaca	1380
accactacac gcagaagagc ctctccctgt ctccgggtaa atgaattc	1428

<210> 91

<211> 758

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide encoding SEQ ID NO: 89

<400> 91

```
aagctttaca gttactcagc acacaggacc tcaccatggg atggagctgt atcatcctct    60
tcttggtagc aacagctaca ggtgtccact ccgatattgt gataaccagc tctccactct    120
ccctgcccgt cacccttgga cagccggcct ccatctcctg caggtctagt aagagtctcc    180
tatataagga tgggaagaca tacttgaatt ggtttcagca gaggccaggc caatctccac    240
agctcctaat ttatttgatg tccaccctg catctggggg cccagacaga ttcagcggcg    300
gtgggtcagg cactgatttc aactgaaaa tcagcagggt ggaggctgag gatgttgggg    360
tttattactg ccaacaactt gtagagtatc cgctcacgtt tggccagggg accaagctgg    420
agatcaaacg tacggtggct gcaccatctg tcttcatctt cccgccatct gatgagcagt    480
tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc agagaggcca    540
aagtacagtg gaagggtggac aacgccctcc aatcgggtaa ctcccaggag agtgtcacag    600
agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg agcaaagcag    660
actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg agctcgcccc    720
tcacaaagag cttcaacagg ggagagtgtt aggaattc    758
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<210> 92

<211> 462

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain sequence for HcLc

<400> 92

```
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1           5           10          15

Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys
20          25          30

Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35          40          45
```


Thr Ser Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 50 55 60

Glu Trp Ile Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn
 65 70 75 80

Glu Lys Phe Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
 85 90 95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110

Tyr Tyr Cys Glu Leu Gly Gln Gly Tyr Trp Gly Gln Gly Thr Leu Val
 115 120 125

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
 130 135 140

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 145 150 155 160

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
 165 170 175

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
 180 185 190

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
 195 200 205

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
 210 215 220

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 225 230 235 240

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
 245 250 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 260 265 270

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
275 280 285

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
290 295 300

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
305 310 315 320

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
325 330 335

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
340 345 350

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
355 360 365

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
370 375 380

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
385 390 395 400

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
405 410 415

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
420 425 430

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
435 440 445

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 93

<211> 1405

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide encoding SEQ ID NO: 92

<400> 93

aagcttgcca ccatgggatg gagctgtatc atcctctttt tggtagcagc agctacaggt	60
gtccactccc aggtccaact gcagcagcct gggactgaac tggatgaagcc tggggcttca	120
gtgaagctgt cctgcaaggc ttctggctac accttcacca gctactggat gcactgggtg	180
aagcagagggc ctggacaagg ccttgagtgg attggaaata ttaatcctag caatgggtgg	240
actaactaca atgagaagtt caagagcaag gccacactga ctgtagacaa atcctccagc	300
acagcctaca tgcagctcag cagcctgaca tctgaggact ctgcgggtcta ttattgtgaa	360
ctgggacagg gctactgggg ccaaggcaca ctagtcacag tctcctcagc ctccaccaag	420
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc	480
ctgggctgcc tggatcaagga ctacttcccc gaaccgggtga cgggtgctgtg gaactcaggg	540
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc	600
ctcagcagcg tggatgaccgt gccctccagc agcttgggca ccagaccta catctgcaac	660
gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttgtgac	720
aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc	780
ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc	840
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc	900
gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt	960
gtggtcagcg tcctcacctg cctgcaccag gactggctga atggcaagga gtacaagtgc	1020
aaggtctcca acaaagccct ccagccccc atcgagaaaa ccatctccaa agccaaaggg	1080
cagccccgag aaccacaggt gtacaccctg ccccatccc gggatgagct gaccaagaac	1140
caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg	1200
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac	1260
ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac	1320
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc	1380
tccctgtctc cgggtaaatg aattc	1405

<210> 94

<211> 239

<212> PRT

<213> Artificial sequence

<220>

<223> Light chain sequence for HcLc

<400> 94

Met Arg Cys Ser Leu Gln Phe Leu Gly Val Leu Met Phe Trp Ile Ser
1 5 10 15

Gly Val Ser Gly Asp Ile Val Ile Thr Gln Asp Glu Leu Ser Asn Pro
20 25 30

Val Thr Ser Gly Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser
35 40 45

Leu Leu Tyr Lys Asp Gly Lys Thr Tyr Leu Asn Trp Phe Leu Gln Arg
50 55 60

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Met Ser Thr Arg Ala
65 70 75 80

Ser Gly Val Ser Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
85 90 95

Thr Leu Glu Ile Ser Arg Val Lys Ala Glu Asp Val Gly Val Tyr Tyr
100 105 110

Cys Gln Gln Leu Val Glu Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys
115 120 125

Leu Glu Leu Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
130 135 140

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
145 150 155 160

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp

165	170	175
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp		
180	185	190
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys		
195	200	205
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln		
210	215	220
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys		
225	230	235

<210> 95

<211> 738

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide encoding SEQ ID NO: 94

<400> 95

aagcttgcca ccatgaggtg ctctcttcag tttctggggg tgcttatgtt ctggatctct	60
ggagtcagtg gggatattgt gataaccag gatgaactct ccaatcctgt cacttctgga	120
gaatcagttt ccatctcctg caggtctagt aagagtctcc tatataagga tgggaagaca	180
tacttgaatt ggtttctgca gagaccagga caatctcctc agctcctgat ctatttgatg	240
tccacccgtg catcaggagt ctcagaccgg tttagtggca gtgggtcagg aacagatttc	300
accctggaaa tcagtagagt gaaggctgag gatgtgggtg tgtattactg tcaacaactt	360
gtagagtatc cgctcacgtt cggtgctggg accaagctgg agctgaaacg tacggtggct	420
gcaccatctg tcttcatctt cccgccatct gatgagcagt tgaaatctgg aactgcctct	480
gttgtgtgcc tgctgaataa cttctatccc agagaggcca aagtacagtg gaaggtggac	540
aacgccctcc aatcggttaa ctcccaggag agtgtcacag agcaggacag caaggacagc	600
acctacagcc tcagcagcac cctgacgctg agcaaagcag actacgagaa acacaaagtc	660
tacgcctgcg aagtcaccca tcagggcctg agctcgcccc tcacaaagag cttcaacagg	720

ggagagtgtt aggaattc

738

<210> 96

<211> 4

<212> PRT

<213> Artificial sequence

<220>

<223> Motif

<400> 96

Tyr Glu Asn Pro
1

<210> 97

<211> 4

<212> PRT

<213> Artificial sequence

<220>

<223> Motif

<400> 97

Lys Lys Gln Asn
1